

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Atkinson, Howard J
 McPherson, Michael J
 Urwin, Peter E
- (ii) TITLE OF INVENTION: Proteinase Inhibitor Fusion Proteins
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Syngenta Biotechnology, Inc.
 - (B) STREET: 3054 Cornwallis Road
 - (C) CITY: RTP
 - (D) STATE: NC
 - (E) COUNTRY: USA
 - (F) ZIP: 27709
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/554,941
 - (B) FILING DATE: 22-MAY-2000
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Meigs, J. Timothy
 - (B) REGISTRATION NUMBER: 38,241
 - (C) REFERENCE/DOCKET NUMBER: S-30287A
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 919-541-8587
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: internal

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PsMTa Linker
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Val Ile Leu Gly Val Gly Pro Ala Lys Ile Gln Phe Glu Gly 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: internal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: galactose oxidase linker
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gln 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: oligo P1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGTCGAGCG ACGGACGGCC GGTGCTTGGC

(2) INFORMATION FOR SEQ ID NO: 4:

	(A) LENGTH: 48 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: oligo P2	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
GATCTTCG	CC GGACCGACGC CAAGAATCAC GGCATTTGCA CTGGCATC	48
(2) INFO	RMATION FOR SEQ ID NO: 5:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: oligo P3	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
GTCGGTCC	GG CGAAGATCCA GTTTGAAGGT AGTAATCATC ATGATGAC	48
(2) INFO	RMATION FOR SEQ ID NO: 6:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	

(i) SEQUENCE CHARACTERISTICS:

	(A) ORGANISM: oligo P4	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
TTCTTACT	CA TCATCTTCAT CCCTGGACTT GC	32
(2) INFO	RMATION FOR SEQ ID NO: 7:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: oligo P5	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
CTGGGGGG	CT GTGTAAGAAC TAGCTTGGGC ATTTGCACTG GCATC	45
(2) INFO	RMATION FOR SEQ ID NO: 8:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: oligo P6	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
AGTTCTTA	CA CAGCCCCCA GCCTGGTAGT AATCATCATG ATGAC	45
(2) INFO	RMATION FOR SEQ ID NO: 9:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: pucleic acid	

(vi) ORIGINAL SOURCE:

	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
ACTATGGAT	C CAGTAATCAT CATGATGACT C	31
(2) INFOR	RMATION FOR SEQ ID NO: 10:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
	SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
ATATTAAGO	CT TTTCTTACTC ATCATCTTC	29
(2) INFOR	RMATION FOR SEQ ID NO: 11:	
. (i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: peptide	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(v)	FRAGMENT TYPE: internal	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: modified galactose oxidase linker	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 11:	

Gln Ala Ser Ile Glu Gly Arg Tyr Thr Ala Pro Gln Pro Gln (2) INFORMATION FOR SEQ ID NO: 12: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: NO (v) FRAGMENT TYPE: internal (vi) ORIGINAL SOURCE: (A) ORGANISM: natural immunoglobulin linker (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12: Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser Leu Asp (2) INFORMATION FOR SEQ ID NO: 13: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: NO (v) FRAGMENT TYPE: internal (vi) ORIGINAL SOURCE: (A) ORGANISM: linker peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Pro 1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: peptide	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(v)	FRAGMENT TYPE: internal	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: linker peptide	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
Gly 1	Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Ser 5 10 15	
(2) INFO	RMATION FOR SEQ ID NO: 15:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: oligo P7	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
ACATGTCG.	AA TTCTTAGGCA TTTGCACTGG C	31
(2) INFO	RMATION FOR SEQ ID NO: 16:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	

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(vi)	ORIGINAL SOURCE: (A) ORGANISM: oligo P8	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 16:	
GAGGAGCC	CCG GGTCGAGCGA CGGA	24
(2) INFO	DRMATION FOR SEQ ID NO: 17:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: oligo P9	
(xi)) SEQUENCE DESCRIPTION: SEQ ID NO: 17:	
CTCGAAC	TCT AGAAGAGAAT TGGCCTTGTT GTG	33
(2) INF	ORMATION FOR SEQ ID NO: 18:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(vi) ORIGINAL SOURCE: (A) ORGANISM: oligo P10	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
AATTCTC	TTC TAGAGTTC	18
(2) INF	ORMATION FOR SEQ ID NO: 19:	

(iii) ANTI-SENSE: NO

	(A) LENGTH: 24 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: oligo P11	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
AAACCATG	GA TGTTCAAGGA GCTC	24
(2) INFO	RMATION FOR SEQ ID NO: 20:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
TCTATCGAZ	AG GTCGC	15
(2) INFO	RMATION FOR SEQ ID NO: 21:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 5 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: peptide	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(v)	FRAGMENT TYPE: internal	

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Ser Ile Glu Gly Arg 1 5